

SEQUENCE LISTING

<110> Ono Pharmaceutical Co., Ltd.

<120> Novel Polypeptides, cDNA coding these polypeptides and Use thereof

<130> ONF-2975PCT

<141> 1999-05-13

<150> JP 10-131815

<151> 1998-05-14

<160> 19

<170> PatentIn Ver. 2.0

<210> 1

<211> 344

<212> PRT

<213> Homo sapiens

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-20

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-10 -5 -1 1

Ser Gly Asp Ala Thr Phe Pro Lys Ala Met Asp Asn Val Thr Val Arg

5 10 15 20

Gln Gly Glu Ser Ala Thr Leu Arg Cys Thr Ile Asp Asn Arg Val Thr

25 30 35

Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu Tyr Ala Gly Asn Asp

40 45 50

Lys Trp Cys Leu Asp Pro Arg Val Val Leu Leu Ser Asn Thr Gln Thr

55 60 65

Gln Tyr Ser Ile Glu Ile Gln Asn Val Asp Val Tyr Asp Glu Gly Pro

70 75 80

Tyr Thr Cys Ser Val Gln Thr Asp Asn His Pro Lys Thr Ser Arg Val

85 90 95 100

His Leu Ile Val Gln Val Ser Pro Lys Ile Val Glu Ile Ser Ser Asp

105 110 115

Ile Ser Ile Asn Glu Gly Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr

120 125 130

Gly Arg Pro Glu Pro Thr Val Thr Trp Arg His Ile Ser Pro Lys Ala

135 140 145

Val Gly Phe Val Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly Ile Thr

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Arg Glu Gln Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val Ala

165 170 175 180

Ala Pro Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr

185

190

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Ile Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr

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210

Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp Tyr

215

220

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Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys Val Glu

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Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val Ser Glu His

245

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Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys Leu Gly His Thr

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Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala Val Ser Glu Val Ser

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Asn Gly Thr Ser Arg Arg Ala Gly Cys Val Trp Leu Leu Pro Leu Leu

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Val Leu His Leu Leu Leu Lys Phe

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<211> 1032

<212> DNA

<213> Homo sapiens

<400> 2

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<213> Homo sapiens

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<222> (130)..(213)

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aaaaaaatc atg aaa acc atc cag cca aaa atg cac aat tct atc tct tgg 171

Met Lys Thr Ile Gln Pro Lys Met His Asn Ser Ile Ser Trp

-25

-20

-15

gca atc ttc acg ggg ctg gct gct ctg tgt ctc ttc caa gga gtg ccc 219

Ala Ile Phe Thr Gly Leu Ala Ala Leu Cys Leu Phe Gln Gly Val Pro

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-5

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Val Arg Ser Gly Asp Ala Thr Phe Pro Lys Ala Met Asp Asn Val Thr

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Val Arg Gln Gly Glu Ser Ala Thr Leu Arg Cys Thr Ile Asp Asn Arg

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gtc acc cgg gtg gcc tgg cta aac cgc agc acc atc ctc tat gct ggg 363

Val Thr Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu Tyr Ala Gly

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aat gac aag tgg tgc ctg gat cct cgc gtg gtc ctt ctg agc aac acc 411

Asn Asp Lys Trp Cys Leu Asp Pro Arg Val Val Leu Leu Ser Asn Thr

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caa acg cag tac agc atc gag atc cag aac gtg gat gtg tat gac gag 459

Gln Thr Gln Tyr Ser Ile Glu Ile Gln Asn Val Asp Val Tyr Asp Glu

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ggc cct tac acc tgc tcg gtg cag aca gac aac cac cca aag acc tct 507

Gly Pro Tyr Thr Cys Ser Val Gln Thr Asp Asn His Pro Lys Thr Ser

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agg gtc cac ctc att gtg caa gta tct ccc aaa att gta gag att tct 555

Arg Val His Leu Ile Val Gln Val Ser Pro Lys Ile Val Glu Ile Ser

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tca gat atc tcc att aat gaa ggg aac aat att agc ctc acc tgc ata 603

Ser Asp Ile Ser Ile Asn Glu Gly Asn Asn Ile Ser Leu Thr Cys Ile

115 120 125 130

gca act ggt aga cca gag cct acg gtt act tgg aga cac atc tct ccc 651

Ala Thr Gly Arg Pro Glu Pro Thr Val Thr Trp Arg His Ile Ser Pro

135 140 145

aaa gcg gtt ggc ttt gtg agt gaa gac gaa tac ttg gaa att cag ggc 699

Lys Ala Val Gly Phe Val Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly

150 155 160

atc acc cgg gag cag tca ggg gac tac gag tgc agt gcc tcc aat gac 747

Ile Thr Arg Glu Gln Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp

165 170 175

gtg gcc gcg ccc gtg gta cgg aga gta aag gtc acc gtg aac tat cca 795

Val Ala Ala Pro Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro

180 185 190

cca tac att tca gaa gcc aag ggt aca ggt gtc ccc gtg gga caa aag 843

Pro Tyr Ile Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys

195 200 205 210

ggg aca ctg cag tgt gaa gcc tca gca gtc ccc tca gca gaa ttc cag 891

Gly Thr Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln

215 220 225

tgg tac aag gat gac aaa aga ctg att gaa gga aag aaa ggg gtg aaa 939

Trp Tyr Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys

230 235 240

gtg gaa aac aga cct ttc ctc tca aaa ctc atc ttc ttc aat gtc tct 987

Val Glu Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val Ser

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gaa cat gac tat ggg aac tac act tgc gtg gcc tcc aac aag ctg ggc 1035

Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys Leu Gly

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cac acc aat gcc agc atc atg cta ttt ggt cca ggc gcc gtc agc gag 1083

His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala Val Ser Glu

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Val Ser Asn Gly Thr Ser Arg Arg Ala Gly Cys Val Trp Leu Leu Pro

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ctt ctg gtc ttg cac ctg ctt ctc aaa ttt tgatgtgagt gccacttccc 1181

Leu Leu Val Leu His Leu Leu Leu Lys Phe

310

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<211> 313

<212> PRT

<213> Homo sapiens

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30

Thr Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu Tyr Ala Gly Asn

35

40

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Asp Lys Trp Cys Leu Asp Pro Arg Val Val Leu Leu Ser Asn Thr Gln

50

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60

Thr Gln Tyr Ser Ile Glu Ile Gln Asn Val Asp Val Tyr Asp Glu Gly

65

70

75

80

Pro Tyr Thr Cys Ser Val Gln Thr Asp Asn His Pro Lys Thr Ser Arg

85

90

95

Val His Leu Ile Val Gln Val Ser Pro Lys Ile Val Glu Ile Ser Ser

100

105

110

Asp Ile Ser Ile Asn Glu Gly Asn Asn Ile Ser Leu Thr Cys Ile Ala

115

120

125

Thr Gly Arg Pro Glu Pro Thr Val Thr Trp Arg His Ile Ser Pro Lys

130

135

140

Ala Val Gly Phe Val Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly Ile

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Thr Arg Glu Gln Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val

165

170

175

Ala Ala Pro Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro

180

185

190

Tyr Ile Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly

195

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Thr Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp

210

215

220

Tyr Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys Val

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235

240

Glu Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val Ser Glu

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His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys Leu Gly His

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Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala Val Ser Glu Val

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Ser Asn Gly Thr Ser Arg Arg Ala Gly Cys Val Trp Leu Leu Pro Leu

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Leu Val Leu His Leu Leu Leu Lys Phe

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<210> 5

<211> 939

<212> DNA

<213> Homo sapiens

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<211> 478

<212> PRT

<213> Homo sapiens

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Val Ile Phe Leu Leu Phe Met Asn Leu Tyr Ile Glu Asp Ser Tyr Val
35 40 45

Leu Glu Gly Asp Lys Gln Leu Ile Arg Glu Thr Ser Thr His Gln Leu
50 55 60

Asn Ser Glu Arg Tyr Val His Thr Phe Lys Asp Leu Ser Asn Phe Ser
65 70 75 80

Gly Ala Ile Asn Val Thr Tyr Arg Tyr Leu Ala Ala Thr Pro Leu Gln
85 90 95

Arg Lys Arg Tyr Leu Thr Ile Gly Leu Ser Ser Val Lys Arg Lys Lys
100 105 110

Gly Asn Tyr Leu Leu Glu Thr Ile Lys Ser Ile Phe Glu Gln Ser Ser
115 120 125

Tyr Glu Glu Leu Lys Glu Ile Ser Val Val Ile His Leu Ala Asp Phe

130

135

140

Asn Ser Ser Trp Arg Asp Ala Met Val Gln Asp Ile Thr Gln Lys Phe

145

150

155

160

Ala His His Ile Ile Ala Gly Arg Leu Met Val Ile His Ala Pro Glu

165

170

175

Glu Tyr Tyr Pro Ile Leu Asp Gly Leu Lys Arg Asn Tyr Asn Asp Pro

180

185

190

Glu Asp Arg Val Lys Phe Arg Ser Lys Gln Asn Val Asp Tyr Thr Phe

195

200

205

Leu Leu Asn Phe Cys Ala Asn Thr Ser Asp Tyr Tyr Val Met Leu Glu

210

215

220

Asp Asp Val Arg Cys Ser Lys Asn Phe Leu Thr Ala Ile Lys Lys Val

225

230

235

240

Ile Ala Ser Leu Glu Gly Thr Tyr Trp Val Thr Leu Glu Phe Ser Lys

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255

Leu Gly Tyr Ile Gly Lys Leu Tyr His Ser His Asp Leu Pro Arg Leu

260

265

270

Ala His Phe Leu Leu Met Phe Tyr Gln Glu Met Pro Cys Asp Trp Leu

275

280

285

Leu Thr His Phe Arg Gly Leu Leu Ala Gln Lys Asn Val Ile Arg Phe

290

295

300

Lys Pro Ser Leu Phe Gln His Met Gly Tyr Tyr Ser Ser Tyr Lys Gly

305

310

315

320

Thr Glu Asn Lys Leu Lys Asp Asp Asp Phe Glu Glu Glu Ser Phe Asp

325

330

335

Ile Pro Asp Asn Pro Pro Ala Ser Leu Tyr Thr Asn Met Asn Val Phe

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Glu Asn Tyr Glu Ala Ser Lys Ala Tyr Ser Ser Val Asp Glu Tyr Phe

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Trp Gly Lys Pro Pro Ser Thr Gly Asp Val Phe Val Ile Val Phe Glu

370

375

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Asn Pro Ile Ile Ile Lys Lys Ile Lys Val Asn Thr Gly Thr Glu Asp

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390

395

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Arg Gln Asn Asp Ile Leu His His Gly Ala Leu Asp Val Gly Glu Asn

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Val Met Pro Ser Lys Gln Arg Gly Gln Cys Ser Thr Tyr Leu Arg Leu

420

425

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Gly Glu Phe Lys Asn Gly Asn Phe Glu Met Ser Gly Val Asn Gln Lys

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440

445

Ile Pro Phe Asp Ile His Cys Met Arg Ile Tyr Val Thr Lys Thr Gln

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Lys Glu Trp Leu Ile Ile Arg Ser Ile Ser Ile Trp Thr Ser

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<211> 1434

<212> DNA

<213> Homo sapiens

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gaaatgtcag gtgtaaatca aaaaattcca ttgatatac attgtatgag gatatatgtc 1380
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<210> 8

<211> 2131

<212> DNA

<213> Homo sapiens

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<223> Clone OM237 derived from human brain

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<221> CDS

<222> (114)..(1547)

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Met

1

ttt aaa ttt cat caa atg aaa cat att ttt gaa ata ctt gat aaa atg 164

Phe Lys Phe His Gln Met Lys His Ile Phe Glu Ile Leu Asp Lys Met

5

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aga tgc ctg aga aaa cgt tct aca gtg tca ttc ttg gga gtt ctt gtc 212

Arg Cys Leu Arg Lys Arg Ser Thr Val Ser Phe Leu Gly Val Leu Val

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30

att ttt ctc ctt ttt atg aac ttg tac att gaa gat agc tat gtt ctg 260

Ile Phe Leu Leu Phe Met Asn Leu Tyr Ile Glu Asp Ser Tyr Val Leu

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gaa gga gac aaa caa ctt ata agg gaa aca tcc aca cat caa ctg aat 308

Glu Gly Asp Lys Gln Leu Ile Arg Glu Thr Ser Thr His Gln Leu Asn

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tca gaa cgc tat gtt cat act ttc aag gat tta tct aat ttc tca gga 356

Ser Glu Arg Tyr Val His Thr Phe Lys Asp Leu Ser Asn Phe Ser Gly

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gcc ata aat gtc acc tat cgc tac cta gct gcc aca cct tta caa aga 404

Ala Ile Asn Val Thr Tyr Arg Tyr Leu Ala Ala Thr Pro Leu Gln Arg

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aag cgg tat ctt aca att gga ctt tct tca gta aag cga aaa aaa gga 452

Lys Arg Tyr Leu Thr Ile Gly Leu Ser Ser Val Lys Arg Lys Lys Gly

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aac tat tta ctt gag aca att aag tca att ttt gag caa tcc agc tat 500

Asn Tyr Leu Leu Glu Thr Ile Lys Ser Ile Phe Glu Gln Ser Ser Tyr

115

120

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gaa gag ctg aag gaa att tca gtg gtg att cac cta gca gac ttt aat 548

Glu Glu Leu Lys Glu Ile Ser Val Val Ile His Leu Ala Asp Phe Asn	
130	135 140 145
tct tcc tgg cgt gat gcc atg gtc cag gat att aca cag aaa ttt gcg	596
Ser Ser Trp Arg Asp Ala Met Val Gln Asp Ile Thr Gln Lys Phe Ala	
150	155 160
cac cat att att gca gga aga tta atg gtt ata cat gct cca gag gag	644
His His Ile Ile Ala Gly Arg Leu Met Val Ile His Ala Pro Glu Glu	
165	170 175
tat tac cca atc cta gat ggc ctt aaa aga aat tac aat gat cca gaa	692
Tyr Tyr Pro Ile Leu Asp Gly Leu Lys Arg Asn Tyr Asn Asp Pro Glu	
180	185 190
gat aga gtc aaa ttt cgt tcc aag caa aat gta gat tat act ttt ctg	740
Asp Arg Val Lys Phe Arg Ser Lys Gln Asn Val Asp Tyr Thr Phe Leu	
195	200 205
ctt aat ttt tgt gcc aat act tca gac tat tat gta atg ctt gaa gat	788
Leu Asn Phe Cys Ala Asn Thr Ser Asp Tyr Tyr Val Met Leu Glu Asp	
210	215 220 225
gat gtt cga tgt tca aaa aat ttc tta act gcc atc aag aaa gtc att	836
Asp Val Arg Cys Ser Lys Asn Phe Leu Thr Ala Ile Lys Lys Val Ile	
230	235 240
gca tcc cta gaa gga act tac tgg gta act ctt gaa ttc tct aag ctt	884
Ala Ser Leu Glu Gly Thr Tyr Trp Val Thr Leu Glu Phe Ser Lys Leu	
245	250 255
ggc tac att ggt aaa ctc tat cat tct cat gat ctc cca cgt ttg gcc	932

Gly Tyr Ile Gly Lys Leu Tyr His Ser His Asp Leu Pro Arg Leu Ala

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265

270

cat ttt tta tta atg ttt tat caa gaa atg cct tgt gat tgg cta ttg 980

His Phe Leu Leu Met Phe Tyr Gln Glu Met Pro Cys Asp Trp Leu Leu

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act cat ttc cgt ggt ctg ttg gct cag aaa aat gtg atc cgt ttt aaa 1028

Thr His Phe Arg Gly Leu Leu Ala Gln Lys Asn Val Ile Arg Phe Lys

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cca tct ctc ttt cag cac atg ggc tat tat tca tca tac aaa ggg acg 1076

Pro Ser Leu Phe Gln His Met Gly Tyr Tyr Ser Ser Tyr Lys Gly Thr

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gag aat aag ctg aag gat gat gat ttt gaa gag gag tca ttt gac att 1124

Glu Asn Lys Leu Lys Asp Asp Asp Phe Glu Glu Glu Ser Phe Asp Ile

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cct gat aac ccc cct gca agt ctg tac acc aac atg aat gtg ttt gaa 1172

Pro Asp Asn Pro Pro Ala Ser Leu Tyr Thr Asn Met Asn Val Phe Glu

340

345

350

aat tat gaa gca agc aag gct tac agt agt gtt gat gag tac ttt tgg 1220

Asn Tyr Glu Ala Ser Lys Ala Tyr Ser Ser Val Asp Glu Tyr Phe Trp

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360

365

ggg aaa cca cct tca aca gga gat gtt ttt gtg att gta ttt gaa aat 1268

Gly Lys Pro Pro Ser Thr Gly Asp Val Phe Val Ile Val Phe Glu Asn

370

375

380

385

cca att ata ata aaa aaa att aaa gta aat act gga aca gaa gat cgg 1316

Pro Ile Ile Ile Lys Lys Ile Lys Val Asn Thr Gly Thr Glu Asp Arg

390

395

400

caa aat gat att ttg cat cat gga gcc cta gat gtt ggg gaa aac gtt 1364

Gln Asn Asp Ile Leu His His Gly Ala Leu Asp Val Gly Glu Asn Val

405

410

415

atg cct agc aaa caa agg gga caa tgt tct act tac tta aga cta gga 1412

Met Pro Ser Lys Gln Arg Gly Gln Cys Ser Thr Tyr Leu Arg Leu Gly

420

425

430

gaa ttc aaa aat gga aac ttt gaa atg tca ggt gta aat caa aaa att 1460

Glu Phe Lys Asn Gly Asn Phe Glu Met Ser Gly Val Asn Gln Lys Ile

435

440

445

cca ttt gat ata cat tgt atg agg ata tat gtc acc aaa aca caa aag 1508

Pro Phe Asp Ile His Cys Met Arg Ile Tyr Val Thr Lys Thr Gln Lys

450

455

460

465

gaa tgg cta att att agg agt att agc att tgg act tct tagccaatta 1557

Glu Trp Leu Ile Ile Arg Ser Ile Ser Ile Trp Thr Ser

470

475

aatcagtatg ttcagtttct gaagcagttc ttcctgcttc gtcttttgct acctttgtct 1617

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tcatttatac attgttgaca taattttact cttaatacac acttgatattt attttaacgt 1737

ctgaagttga atatcagtct atagctaagt ctactttcat ttatatattt aaatgttctt 1797

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tttgttggat gatgattttt gaaaaatagt caccaactgt atatacttcc tcaagaactg 1917

ataattcatt atatcatcag atagctttta ttaagcatct gtgggaatat acagttgggt 1977

ggaatgataa tctggtttat tttttctgta aacttaagtt tccgttgact tctgtacatc 2037
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tatggaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 2131

<210> 9

<211> 335

<212> PRT

<213> Homo sapiens

<400> 9

Met Asp Ser Ala Leu Ser Asp Pro His Asn Gly Ser Ala Glu Ala Gly

1 5 10 15

Gly Pro Thr Asn Ser Thr Thr Arg Pro Pro Ser Thr Pro Glu Gly Ile

20 25 30

Ala Leu Ala Tyr Gly Ser Leu Leu Leu Met Ala Leu Leu Pro Ile Phe

35 40 45

Phe Gly Ala Leu Arg Ser Val Arg Cys Ala Arg Gly Lys Asn Ala Ser

50 55 60

Asp Met Pro Glu Thr Ile Thr Ser Arg Asp Ala Ala Arg Phe Pro Ile

65 70 75 80

Ile Ala Ser Cys Thr Leu Leu Gly Leu Tyr Leu Phe Phe Lys Ile Phe

85 90 95

Ser Gln Glu Tyr Ile Asn Leu Leu Leu Ser Met Tyr Phe Phe Val Leu

100	105	110	
Gly Ile Leu Ala Leu Ser His Thr Ile Ser Pro Phe Met Asn Lys Phe			
115	120	125	
Phe Pro Ala Ser Phe Pro Asn Arg Gln Tyr Gln Leu Leu Phe Thr Gln			
130	135	140	
Gly Ser Gly Glu Asn Lys Glu Glu Ile Ile Asn Tyr Glu Phe Asp Thr			
145	150	155	160
Lys Asp Leu Val Cys Leu Gly Leu Ser Ser Ile Val Gly Val Trp Tyr			
165	170	175	
Leu Leu Arg Lys Val Phe Gly Thr Asn Val Met Val Thr Val Ala Lys			
180	185	190	
Ser Phe Glu Ala Pro Ile Lys Leu Val Phe Pro Gln Asp Leu Leu Glu			
195	200	205	
Lys Gly Leu Glu Ala Asn Asn Phe Ala Met Leu Gly Leu Gly Asp Val			
210	215	220	
Val Ile Pro Gly Ile Phe Ile Ala Leu Leu Leu Arg Phe Asp Ile Ser			
225	230	235	240
Leu Lys Lys Asn Thr His Thr Tyr Phe Tyr Thr Ser Phe Ala Ala Tyr			
245	250	255	
Ile Phe Gly Leu Gly Leu Thr Ile Phe Ile Met His Ile Phe Lys His			
260	265	270	
Ala Gln Pro Ala Leu Leu Tyr Leu Val Pro Ala Cys Ile Gly Phe Pro			
275	280	285	
Val Leu Val Ala Leu Ala Lys Gly Glu Val Thr Glu Met Phe Ser Tyr			

290	295	300	
Glu Glu Ser Asn Pro Lys Asp Pro Ala Ala Val Thr Glu Ser Lys Glu			
305	310	315	320
Gly Thr Glu Ala Ser Ala Ser Lys Gly Leu Glu Lys Lys Glu Lys			
	325	330	335

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<211> 1005

<212> DNA

<213> Homo sapiens

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aaggacctgg tgtgcctggg cctgagcagc atcggtggcg tctggtacct gctgaggaag 540
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gtgtttcccc aggatctgct ggagaaagge ctggaagcaa acaactttgc catgctggga 660

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<210> 11

<211> 1486

<212> DNA

<213> Homo sapiens

<220>

<223> Clone OA004b derived from T98G cell

<220>

<221> CDS

<222> (117)..(1121)

<400> 11

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Met

gac tcg gcc ctc agc gat ccg cat aac ggc agt gcc gag gca ggc ggc 167

Asp Ser Ala Leu Ser Asp Pro His Asn Gly Ser Ala Glu Ala Gly Gly

5

10

15

ccc acc aac agc act acg cgg ccg cct tcc acg ccc gag ggc atc gcg 215

Pro Thr Asn Ser Thr Thr Arg Pro Pro Ser Thr Pro Glu Gly Ile Ala

20

25

30

ctg gcc tac ggc agc ctc ctg ctc atg gcg ctg ctg ccc atc ttc ttc 263

Leu Ala Tyr Gly Ser Leu Leu Leu Met Ala Leu Leu Pro Ile Phe Phe

35

40

45

ggc gcc ctg cgc tcc gta cgc tgc gcc cgc ggc aag aat gct tca gac 311

Gly Ala Leu Arg Ser Val Arg Cys Ala Arg Gly Lys Asn Ala Ser Asp

50

55

60

65

atg cct gaa aca atc acc agc cgg gat gcc gcc cgc ttc ccc atc atc 359

Met Pro Glu Thr Ile Thr Ser Arg Asp Ala Ala Arg Phe Pro Ile Ile

70

75

80

gcc agc tgc aca ctc ttg ggg ctc tac ctc ttt ttc aaa ata ttc tcc 407

Ala Ser Cys Thr Leu Leu Gly Leu Tyr Leu Phe Phe Lys Ile Phe Ser

85

90

95

cag gag tac atc aac ctc ctg ctg tcc atg tat ttc ttc gtg ctg gga 455

Gln Glu Tyr Ile Asn Leu Leu Leu Ser Met Tyr Phe Phe Val Leu Gly

100

105

110

atc ctg gcc ctg tcc cac acc atc agc ccc ttc atg aat aag ttt ttt 503

Ile Leu Ala Leu Ser His Thr Ile Ser Pro Phe Met Asn Lys Phe Phe

115	120	125	
cca gcc agc ttt cca aat cga cag tac cag ctg ctc ttc aca cag ggt	551		
Pro Ala Ser Phe Pro Asn Arg Gln Tyr Gln Leu Leu Phe Thr Gln Gly			
130	135	140	145
tct ggg gaa aac aag gaa gag atc atc aat tat gaa ttt gac acc aag	599		
Ser Gly Glu Asn Lys Glu Glu Ile Ile Asn Tyr Glu Phe Asp Thr Lys			
	150	155	160
gac ctg gtg tgc ctg ggc ctg agc agc atc gtt ggc gtc tgg tac ctg	647		
Asp Leu Val Cys Leu Gly Leu Ser Ser Ile Val Gly Val Trp Tyr Leu			
	165	170	175
ctg agg aag gta ttt ggc acc aat gtg atg gtg aca gtg gcc aag tcc	695		
Leu Arg Lys Val Phe Gly Thr Asn Val Met Val Thr Val Ala Lys Ser			
	180	185	190
ttc gag gca cca ata aaa ttg gtg ttt ccc cag gat ctg ctg gag aaa	743		
Phe Glu Ala Pro Ile Lys Leu Val Phe Pro Gln Asp Leu Leu Glu Lys			
	195	200	205
ggc ctc gaa gca aac aac ttt gcc atg ctg gga ctt gga gat gtc gtc	791		
Gly Leu Glu Ala Asn Asn Phe Ala Met Leu Gly Leu Gly Asp Val Val			
210	215	220	225
att cca ggg atc ttc att gcc ttg ctg ctg cgc ttt gac atc agc ttg	839		
Ile Pro Gly Ile Phe Ile Ala Leu Leu Leu Arg Phe Asp Ile Ser Leu			
	230	235	240
aag aag aat acc cac acc tac ttc tac acc agc ttt gca gcc tac atc	887		
Lys Lys Asn Thr His Thr Tyr Phe Tyr Thr Ser Phe Ala Ala Tyr Ile			

245	250	255	
ttc ggc ctg ggc ctt acc atc ttc atc atg cac atc ttc aag cat gct			935
Phe Gly Leu Gly Leu Thr Ile Phe Ile Met His Ile Phe Lys His Ala			
260	265	270	
cag cct gcc ctc cta tac ctg gtc ccc gcc tgc atc ggt ttt cct gtc			983
Gln Pro Ala Leu Leu Tyr Leu Val Pro Ala Cys Ile Gly Phe Pro Val			
275	280	285	
ctg gtg gcg ctg gcc aag gga gaa gtg aca gag atg ttc agt tat gag			1031
Leu Val Ala Leu Ala Lys Gly Glu Val Thr Glu Met Phe Ser Tyr Glu			
290	295	300	305
gag tca aat cct aag gat cca gcg gca gtg aca gaa tcc aaa gag gga			1079
Glu Ser Asn Pro Lys Asp Pro Ala Ala Val Thr Glu Ser Lys Glu Gly			
310	315	320	
aca gag gca tca gca tcg aag ggg ctg gag aag aaa gag aaa			1121
Thr Glu Ala Ser Ala Ser Lys Gly Leu Glu Lys Lys Glu Lys			
325	330	335	
tgatgcggct ggtgcccag cctctcaggg ccagaccaga cagatggggg ctgggcccac			1181
acaggcgtgc accggtagag ggcacaggag gccaaaggca gctccaggac agggcagggg			1241
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aaaaa			1486

<210> 12

<211> 360

<212> PRT

<213> Homo sapiens

<400> 12

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-15

-10

-5

-1

Gly Gln Glu Lys Phe Phe Gly Asp Gln Val Phe Arg Ile Asn Val Arg

1

5

10

15

Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn Ser Asn Asn

20

25

30

Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe Asn Arg Pro Val

35

40

45

Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala Phe Lys Ser Phe Leu

50

55

60

Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr Ile Glu Asp Leu Gln Ala

65

70

75

80

Leu Leu Asp Asn Glu Asp Asp Glu Met Gln His Asn Glu Gly Gln Glu

85

90

95

Arg Ser Ser Asn Asn Phe Asn Tyr Gly Ala Tyr His Ser Leu Glu Ala

100

105

110

Ile Tyr His Glu Met Asp Asn Ile Ala Ala Asp Phe Pro Asp Leu Ala

115	120	125	
Arg Arg Val Lys Ile Gly His Ser Phe Glu Asn Arg Pro Met Tyr Val			
130	135	140	
Leu Lys Phe Ser Thr Gly Lys Gly Val Arg Arg Pro Ala Val Trp Leu			
145	150	155	160
Asn Ala Gly Ile His Ser Arg Glu Trp Ile Ser Gln Ala Thr Ala Ile			
165	170	175	
Trp Thr Ala Arg Lys Ile Val Ser Asp Tyr Gln Arg Asp Pro Ala Ile			
180	185	190	
Thr Ser Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro Val Ala Asn			
195	200	205	
Pro Asp Gly Tyr Val Tyr Thr Gln Thr Gln Asn Arg Leu Trp Arg Lys			
210	215	220	
Thr Arg Ser Arg Asn Pro Gly Ser Ser Cys Ile Gly Ala Asp Pro Asn			
225	230	235	240
Arg Ser Trp Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser Asp Asn Pro			
245	250	255	
Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu Val Glu Val			
260	265	270	
Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn Phe Lys Cys Phe			
275	280	285	
Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met Tyr Pro Tyr Gly Tyr			
290	295	300	
Ser Val Lys Lys Ala Pro Asp Ala Glu Glu Leu Asp Lys Val Ala Arg			

305	310	315	320
Leu	Ala	Ala	Lys
Ala	Leu	Ala	Ser
Val	Ser	Gly	Thr
Glu	Tyr	Gln	Val
325	330	335	
Gly	Pro	Thr	Cys
Thr	Thr	Val	Leu
340			

<210> 13

<211> 1080

<212> DNA

<213> Homo sapiens

<400> 13

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agtcaactag tgaattcaaa caacttgaag ctcaatttct ggaaatctcc ctctccttc 180
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<210> 14

<211> 3156

<212> DNA

<213> Homo sapiens

<220>

<223> Clone OAF075b derived from human bone marrow stroma cell HAS303

<220>

<221> CDS

<222> (11)..(1090)

<220>

<221> sig_peptide

<222> (11)..(58)

<220>

<221> mat_peptide

<222> (59)..(1090)

<400> 14

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Met Arg Trp Ile Leu Phe Ile Gly Ala Leu Ile Gly Ser

-15

-10

-5

agc atc tgt ggc caa gaa aaa ttt ttt ggg gac caa gtt ttt agg att 97

Ser Ile Cys Gly Gln Glu Lys Phe Phe Gly Asp Gln Val Phe Arg Ile

-1 1

5

10

aat gtc aga aat gga gac gag atc agc aaa ttg agt caa cta gtg aat 145

Asn Val Arg Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn

15

20

25

tca aac aac ttg aag ctc aat ttc tgg aaa tct ccc tcc tcc ttc aat 193

Ser Asn Asn Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe Asn

30

35

40

45

cgg cct gtg gat gtc ctg gtc cca tct gtc agt ctg cag gca ttt aaa 241

Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala Phe Lys

50

55

60

tcc ttc ctg aga tcc cag ggc tta gag tac gca gtg aca att gag gac 289

Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr Ile Glu Asp

65

70

75

ctg cag gcc ctt tta gac aat gaa gat gat gaa atg caa cac aat gaa 337

Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met Gln His Asn Glu

80

85

90

ggg caa gaa cgg agc agt aat aac ttc aac tac ggg gct tac cat tcc 385

Gly Gln Glu Arg Ser Ser Asn Asn Phe Asn Tyr Gly Ala Tyr His Ser

95

100

105

ctg gaa gct att tac cac gag atg gac aac att gcc gca gac ttt cct 433

Leu Glu Ala Ile Tyr His Glu Met Asp Asn Ile Ala Ala Asp Phe Pro

110

115

120

125

gac ctg gcg agg agg gtg aag att gga cat tcg ttt gaa aac cgg ccg 481

Asp Leu Ala Arg Arg Val Lys Ile Gly His Ser Phe Glu Asn Arg Pro

130

135

140

atg tat gta ctg aag ttc agc act ggg aaa ggc gtg agg cgg ccg gcc 529

Met Tyr Val Leu Lys Phe Ser Thr Gly Lys Gly Val Arg Arg Pro Ala

145

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155

gtt tgg ctg aat gca ggc atc cat tcc cga gag tgg atc tcc cag gcc 577

Val Trp Leu Asn Ala Gly Ile His Ser Arg Glu Trp Ile Ser Gln Ala

160

165

170

act gca atc tgg acg gca agg aag att gta tct gat tac cag agg gat 625

Thr Ala Ile Trp Thr Ala Arg Lys Ile Val Ser Asp Tyr Gln Arg Asp

175

180

185

cca gct atc acc tcc atc ttg gag aaa atg gat att ttc ttg ttg cct 673

Pro Ala Ile Thr Ser Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro

190

195

200

205

gtg gcc aat cct gat gga tat gtg tat act caa act caa aac cga tta 721

Val Ala Asn Pro Asp Gly Tyr Val Tyr Thr Gln Thr Gln Asn Arg Leu

210

215

220

tgg agg aag acg cgg tcc cga aat cct gga agc tcc tgc att ggt gct 769

Trp Arg Lys Thr Arg Ser Arg Asn Pro Gly Ser Ser Cys Ile Gly Ala

225

230

235

gac cca aat aga agc tgg aac gct agt ttt gca gga aag gga gcc agc 817

Asp Pro Asn Arg Ser Trp Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser

240

245

250

gac aac cct tgc tcc gaa gtg tac cat gga ccc cac gcc aat tcg gaa 865

Asp Asn Pro Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu

255

260

265

gtg gag gtg aaa tca gtg gta gat ttc atc caa aaa cat ggg aat ttc 913

Val Glu Val Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn Phe

270

275

280

285

aag tgc ttc atc gac ctg cac agc tac tcg cag ctg ctg atg tat cca 961

Lys Cys Phe Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met Tyr Pro

290

295

300

tat ggg tac tca gtc aaa aag gcc cca gat gcc gag gaa ctc gac aag 1009

Tyr Gly Tyr Ser Val Lys Lys Ala Pro Asp Ala Glu Glu Leu Asp Lys

305

310

315

gtg gcg agg ctt gcg gcc aaa gct ctg gct tct gtg tcg ggc act gag 1057

Val Ala Arg Leu Ala Ala Lys Ala Leu Ala Ser Val Ser Gly Thr Glu

320

325

330

tac caa gtg ggt ccc acc tgc acc act gtc tta taaactgccaa aaactgggag 1110

Tyr Gln Val Gly Pro Thr Cys Thr Thr Val Leu

335

340

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 aaaaaa 3156

<210> 15

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 15

cgattgaatt ctagacctgc ctgagnnnn nnnnn

<210> 16

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer OC001-F1

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27

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<223> Description of Artificial Sequence:Primer OAF075-F1

<400> 19

ccccggggac atgaggtgga tactgtt

27

NAME	ADDRESS	CITY	STATE	ZIP
Mr. J. H. Smith	123 Main St.	Springfield	Ill.	62761
Mr. W. R. Jones	456 Oak Ave.	Chicago	Ill.	60601
Mr. T. L. Brown	789 Elm St.	Peoria	Ill.	61601
Mr. S. K. White	101 Maple Dr.	Rockford	Ill.	61101
Mr. M. D. Green	202 Pine St.	Decatur	Ill.	62521
Mr. L. P. Black	303 Cedar Ave.	Normal	Ill.	62451
Mr. R. G. Gray	404 Birch St.	Urbana	Ill.	61501
Mr. H. J. King	505 Walnut Dr.	Champaign	Ill.	61821
Mr. F. I. Hall	606 Spruce Ave.	Carbondale	Ill.	62901
Mr. D. E. Young	707 Ash St.	Macomb	Ill.	61451
Mr. C. B. Allen	808 Hickory Dr.	Edwardsville	Ill.	62021
Mr. N. M. Wright	909 Sycamore Ave.	St. Louis	Mo.	63101
Mr. K. L. Scott	1010 Chestnut St.	St. Louis	Mo.	63101
Mr. J. M. Adams	1111 Locust Ave.	St. Louis	Mo.	63101
Mr. P. H. Baker	1212 Olive St.	St. Louis	Mo.	63101
Mr. Q. W. Carter	1313 Madison St.	St. Louis	Mo.	63101
Mr. R. T. Evans	1414 Franklin St.	St. Louis	Mo.	63101
Mr. S. U. Foster	1515 Washington St.	St. Louis	Mo.	63101
Mr. T. V. Gibson	1616 Jefferson St.	St. Louis	Mo.	63101
Mr. U. W. Harlan	1717 Adams St.	St. Louis	Mo.	63101
Mr. V. X. Hill	1818 Monroe St.	St. Louis	Mo.	63101
Mr. W. Y. Jordan	1919 Taylor St.	St. Louis	Mo.	63101
Mr. X. Z. Long	2020 Lincoln St.	St. Louis	Mo.	63101
Mr. Y. A. Perry	2121 Jackson St.	St. Louis	Mo.	63101
Mr. Z. B. Reed	2222 Grant St.	St. Louis	Mo.	63101
Mr. A. C. Stewart	2323 Hayes St.	St. Louis	Mo.	63101
Mr. B. D. Thomas	2424 Polk St.	St. Louis	Mo.	63101
Mr. C. E. Turner	2525 Cass St.	St. Louis	Mo.	63101
Mr. D. F. Walker	2626 Erie St.	St. Louis	Mo.	63101
Mr. E. G. Young	2727 Main St.	St. Louis	Mo.	63101
Mr. F. H. Allen	2828 Market St.	St. Louis	Mo.	63101
Mr. G. I. Baker	2929 Chestnut St.	St. Louis	Mo.	63101
Mr. H. J. Carter	3030 Olive St.	St. Louis	Mo.	63101
Mr. I. K. Evans	3131 Madison St.	St. Louis	Mo.	63101
Mr. J. L. Foster	3232 Franklin St.	St. Louis	Mo.	63101
Mr. K. M. Gibson	3333 Washington St.	St. Louis	Mo.	63101
Mr. L. N. Harlan	3434 Jefferson St.	St. Louis	Mo.	63101
Mr. M. O. Hill	3535 Adams St.	St. Louis	Mo.	63101
Mr. N. P. Jordan	3636 Monroe St.	St. Louis	Mo.	63101
Mr. O. Q. Long	3737 Taylor St.	St. Louis	Mo.	63101
Mr. P. R. Perry	3838 Lincoln St.	St. Louis	Mo.	63101
Mr. Q. S. Reed	3939 Jackson St.	St. Louis	Mo.	63101
Mr. R. T. Stewart	4040 Grant St.	St. Louis	Mo.	63101
Mr. S. U. Thomas	4141 Hayes St.	St. Louis	Mo.	63101
Mr. T. V. Turner	4242 Polk St.	St. Louis	Mo.	63101
Mr. U. W. Walker	4343 Cass St.	St. Louis	Mo.	63101
Mr. V. X. Young	4444 Erie St.	St. Louis	Mo.	63101
Mr. W. Y. Allen	4545 Main St.	St. Louis	Mo.	63101
Mr. X. Z. Baker	4646 Market St.	St. Louis	Mo.	63101
Mr. Y. A. Carter	4747 Chestnut St.	St. Louis	Mo.	63101
Mr. Z. B. Evans	4848 Olive St.	St. Louis	Mo.	63101
Mr. A. C. Foster	4949 Madison St.	St. Louis	Mo.	63101
Mr. B. D. Gibson	5050 Franklin St.	St. Louis	Mo.	63101
Mr. C. E. Harlan	5151 Washington St.	St. Louis	Mo.	63101
Mr. D. F. Hill	5252 Jefferson St.	St. Louis	Mo.	63101
Mr. E. G. Jordan	5353 Adams St.	St. Louis	Mo.	63101
Mr. F. H. Long	5454 Monroe St.	St. Louis	Mo.	63101
Mr. G. I. Perry	5555 Taylor St.	St. Louis	Mo.	63101
Mr. H. J. Reed	5656 Lincoln St.	St. Louis	Mo.	63101
Mr. I. K. Stewart	5757 Jackson St.	St. Louis	Mo.	63101
Mr. J. L. Thomas	5858 Grant St.	St. Louis	Mo.	63101
Mr. K. M. Turner	5959 Hayes St.	St. Louis	Mo.	63101
Mr. L. N. Walker	6060 Polk St.	St. Louis	Mo.	63101
Mr. M. O. Young	6161 Cass St.	St. Louis	Mo.	63101
Mr. N. P. Allen	6262 Erie St.	St. Louis	Mo.	63101
Mr. O. Q. Baker	6363 Main St.	St. Louis	Mo.	63101
Mr. P. R. Carter	6464 Market St.	St. Louis	Mo.	63101
Mr. Q. S. Evans	6565 Chestnut St.	St. Louis	Mo.	63101
Mr. R. T. Foster	6666 Olive St.	St. Louis</		